

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/734,782A  
Source: 1Fw/b  
Date Processed by STIC: 4/21/06

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 04/21/2006

PATENT APPLICATION: US/10/734,782A

TIME: 12:53:10

Input Set : A:\SEQLIST.TXT

Output Set: N:\CRF4\04212006\J734782A.raw

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4 <110> APPLICANT: Griffiths, Steven
5   Ritchie, Rachael Jane
7 <120> TITLE OF INVENTION: Nucleic Acid And Amino Acid Sequences Of
8   Infectious Salmon Anaemia Virus And Their Uses As Vaccines
11 <130> FILE REFERENCE: H-32318B
13 <140> CURRENT APPLICATION NUMBER: US 10/734,782A
C--> 14 <141> CURRENT FILING DATE: 2004-04-02
16 <150> PRIOR APPLICATION NUMBER: US 10/049,086
17 <151> PRIOR FILING DATE: 2002-02-06
19 <150> PRIOR APPLICATION NUMBER: PCT/GB00/02976
20 <151> PRIOR FILING DATE: 2000-08-07
22 <150> PRIOR APPLICATION NUMBER: GB 0006674.6
23 <151> PRIOR FILING DATE: 2000-03-21
25 <150> PRIOR APPLICATION NUMBER: GB 0005848.7
26 <151> PRIOR FILING DATE: 2000-03-11
28 <150> PRIOR APPLICATION NUMBER: GB 9918588.6
29 <151> PRIOR FILING DATE: 1999-08-07
31 <160> NUMBER OF SEQ ID NOS: 10
33 <170> SOFTWARE: FastSEQ for Windows Version 4.0
35 <210> SEQ ID NO: 1
36 <211> LENGTH: 1821
37 <212> TYPE: DNA
38 <213> ORGANISM: Infectious Salmon Anaemia Virus
40 <400> SEQUENCE: 1
41 caagatggat aacctccgtg aatgcataaa ccgcaaaaga agactacttg ccttaccaga 60
42 tgttcctgaa acttcggatg ccttttctaag tgatttgaga catctataca tgtgtgttgc 120
43 tttctgtgat caacacaaaa ccactggaga cgaatcaaga ttcaccaacc tggaattact 180
44 tgaccaagat gaagcactag gtgcccacaa agcttttgaa gccaaacatg gaataaaagg 240
45 aggttcttta ggagacgttc ttgacctaga actgaaaaag gtcattgaat ttactttttac 300
46 ttctggaagt ttgtatattg ccgaacaaaag aaaaagaaaag actcaagcag actcaataat 360
47 tgtgtgctgt tcagaaggac ttaacgactt cagcgtatca cacggagtgc tagacatggg 420
48 acttgtggaa acaggggtga atgcagtaag agatttctgc acacaaaacg gaataccaat 480
49 gaagataaat caggtaggat ccacgagaa acacacaccg atcagcacat gcaaaatctc 540
50 tgaacaaata acacgacaga taaacagtac aattactgaa aggaaaatgg aaacagtact 600
51 ggcagcaatc gcaattaaac cagaactcaa actaactcag aaaggatgca gaccttgtaa 660
52 agaactagaa gatgaaaata ttctgtggat ggacctcaa ttctgtgaaa ttgatgaaag 720
53 ttttccttac agaggagggc catacgggaa cttcctgcaa gaattgctgc ttacaaccaa 780
54 cgacttagag accaacggga aagacagaga agaagtagta aagaagatac tggataacaa 840
55 ggcgttcacc gttgaaagtg gtgaatgcat aataacactt ccagacaaaa tgacttggtt 900
56 cggagaacag gagaagaaga gaccagcaac aatagacgaa gtgagaaccg caggagaaag 960
57 gtttgaacag agtggttaac cgaaaaccca aagatatgga aggttatcag acaaattggat 1020
58 ggagcttgaa aagtttatct ttactgcaag caaacagaa gtggatactt tcctttctgt 1080
59 agggaccgaa agacttgagt cggttggagt gtgtgtcgga gctttacaca gagcgaccac 1140

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60 aaccaggata attagaccta tgattcaagg agggaaatgt tgggggatga tgttcaaaac 1200
61 aaagtccaaa atgggagaca cgaggaagga aggatactgt cacgcaatca ttttcggaaa 1260
62 aggggaagat aaatcaggac aaaacaagat gacaatgatg gggaaaacag tacattggca 1320
63 tctaagagta gttaagtcta aaggagactg gatggcgcaa caactctgtg caaacaaaag 1380
64 cagaatatgg gaacatgacc ctgagctagt aacagaagga gtgacagttc taatgacgcc 1440
65 tttttctcag aaaattgccca ccattagtag atggaggggca atgaggttag acagcatgtt 1500
66 tcatgtttct agtgccctggc atcattcacc tgcgtgtgaa gctgcatcgg caatgctgag 1560
67 aaagtttgtg gagatagtag atgccatcaa ccagaaaaga gattgggggtg ttgtggggag 1620
68 tatggaggac atggtgaagg aagtggagga aataggggag cacttgcaga cggcatgtga 1680
69 ttttagagtt tacaacatgt gcaaagcctt gattcagaaa attgcagtca gtacccaatg 1740
70 agtggttatt tacttgtaaa ttgtgtgtg tttgacgata tgtatttgtc gacgcggccg 1800
71 cggtcgacgc ggccgcgaat t 1821

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73 &lt;210&gt; SEQ ID NO: 2

74 &lt;211&gt; LENGTH: 578

75 &lt;212&gt; TYPE: PRT

76 &lt;213&gt; ORGANISM: Infectious Salmon Anaemia Virus

78 &lt;400&gt; SEQUENCE: 2

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79 Met Asp Asn Leu Arg Glu Cys Ile Asn Arg Lys Arg Arg Leu Leu Ala
80 1 5 10 15
81 Leu Pro Asp Val Pro Glu Thr Ser Asp Ala Phe Leu Ser Asp Leu Arg
82 20 25 30
83 His Leu Tyr Met Cys Val Ala Phe Cys Asp Gln His Lys Thr Thr Gly
84 35 40 45
85 Asp Glu Ser Arg Phe Thr Asn Leu Glu Leu Leu Asp Gln Asp Glu Ala
86 50 55 60
87 Leu Gly Ala Gln Arg Ala Phe Glu Ala Lys His Gly Ile Lys Gly Gly
88 65 70 75 80
89 Ser Leu Gly Asp Val Leu Asp His Glu Leu Lys Lys Val Ile Glu Phe
90 85 90 95
91 Thr Phe Thr Ser Gly Ser Leu Tyr Ile Ala Glu Gln Arg Lys Arg Lys
92 100 105 110
93 Thr Gln Ala Asp Ser Ile Ile Val Cys Val Ser Glu Gly Leu Asn Asp
94 115 120 125
95 Phe Ser Val Ser His Gly Val Leu Asp Met Gly Leu Val Glu Thr Gly
96 130 135 140
97 Val Asn Ala Val Arg Asp Phe Cys Thr Gln Asn Gly Ile Pro Met Lys
98 145 150 155 160
99 Ile Asn Gln Val Gly Ser Thr Arg Thr Pro Thr Pro Ile Ser Thr Cys
100 165 170 175
101 Lys Ile Ser Glu Gln Ile Thr Arg Gln Ile Asn Ser Thr Ile Thr Glu
102 180 185 190
103 Arg Lys Met Glu Thr Val Leu Ala Ala Ile Ala Ile Lys Pro Glu Leu
104 195 200 205
105 Lys Leu Thr Gln Lys Gly Cys Arg Pro Cys Lys Glu Leu Glu Asp Glu
106 210 215 220
107 Asn Ile Leu Trp Met Asp Pro Gln Phe Cys Glu Ile Asp Glu Ser Phe
108 225 230 235 240
109 Pro Tyr Arg Gly Gly Pro Tyr Gly Asn Phe Leu Gln Glu Leu Leu Leu
110 245 250 255

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111 Thr Thr Asn Asp Val Glu Thr Asn Gly Lys Asp Arg Glu Glu Val Val
112          260          265          270
113 Lys Lys Ile Leu Asp Asn Lys Ala Phe Thr Val Glu Ser Gly Glu Cys
114          275          280          285
115 Ile Ile Thr Leu Pro Asp Lys Met Thr Cys Phe Gly Glu Gln Glu Lys
116          290          295          300
117 Lys Arg Pro Ala Thr Ile Asp Glu Val Arg Thr Ala Gly Glu Arg Phe
118 305          310          315          320
119 Glu Gln Ser Val Lys Pro Lys Thr Gln Arg Tyr Gly Arg Leu Ser Asp
120          325          330          335
121 Lys Trp Met Glu Leu Glu Lys Phe Ile Phe Thr Ala Ser Lys Thr Glu
122          340          345          350
123 Val Asp Thr Phe Leu Ser Val Gly Thr Glu Arg Leu Glu Ser Val Gly
124          355          360          365
125 Val Cys Val Gly Ala Leu His Arg Ala Thr Thr Thr Arg Ile Ile Arg
126          370          375          380
127 Pro Met Ile Gln Gly Gly Lys Cys Trp Gly Met Met Phe Lys Thr Lys
128 385          390          395          400
129 Ser Lys Met Gly Asp Thr Arg Lys Glu Gly Tyr Cys His Ala Ile Ile
130          405          410          415
131 Phe Gly Lys Gly Glu Asp Lys Ser Gly Gln Asn Lys Met Thr Met Met
132          420          425          430
133 Gly Lys Thr Val His Trp His Leu Arg Val Val Lys Ser Lys Gly Asp
134          435          440          445
135 Trp Met Ala Gln Gln Leu Cys Ala Asn Lys Ser Arg Ile Trp Glu His
136          450          455          460
137 Asp Pro Glu Leu Val Thr Glu Gly Val Thr Val Leu Met Thr Pro Phe
138 465          470          475          480
139 Ser Gln Lys Ile Ala Thr Ile Ser Arg Trp Arg Ala Met Arg Leu Asp
140          485          490          495
141 Ser Met Phe His Val Ser Ser Ala Trp His His Ser Pro Ala Cys Glu
142          500          505          510
143 Ala Ala Ser Ala Met Leu Arg Lys Phe Val Glu Ile Val His Ala Ile
144          515          520          525
145 Asn Gln Lys Arg Asp Trp Gly Val Val Gly Ser Met Glu Asp Met Val
146          530          535          540
147 Lys Glu Val Glu Glu Ile Gly Glu His Leu Gln Thr Ala Cys Asp Phe
148 545          550          555          560
149 Arg Val Tyr Asn Met Cys Lys Ala Leu Ile Gln Lys Ile Ala Val Ser
150          565          570          575
151 Thr Gln
155 <210> SEQ ID NO: 3
156 <211> LENGTH: 2018
157 <212> TYPE: DNA
158 <213> ORGANISM: Infectious Salmon Anaemia Virus
160 <400> SEQUENCE: 3
161 gcaaagatyg ctcaaattccc aaaaataata cagaaaacgt ataagagatg gccgataaag 60
162 gtatgactta ttcttttgat gtcagagaca acaccttggt tgtaagaaga tctaccgcta 120
163 ctaaaagtgg cattaagatc tcctacagag aggatcgagg aacatcactt ctccaaaagg 180

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164 cattcgccgg gacagaagat gaattctggg tggagttaga tcaagatgtc tacgttgaca 240
165 aaaagattag aaaattcctg gaagaagaga aaatgaagga catgagcaca agagtgtctg 300
166 gagcagtggc agcagcaatt gaaagatcag ttgaatttga caatttctca aaagaagcag 360
167 cagctaacat tgaaatggct ggtgtagatg atgaagaagc tggaggaagt ggtctggtag 420
168 acaacagaag gaagaacaaa ggggtctcaa acatggccta caatctgtct ctattcatag 480
169 ggatggtggt tcctgctctc actactttct tcagtgtat cctatcagaa ggtgaaatga 540
170 gcatctggca aaatggacaa gcaatcatca gaattctggc actggcagat gaagacggaa 600
171 agagacaaac aagaacagga ggacagaggg tggacatggc tgatgtaacc aagctgaacg 660
172 tagtcacggc taacgggaaa gtcaagcaag ttgaagtaaa cttgaacgat ctcaaagcag 720
173 cattcaggca gagtagacct aaaagatcgg actacagaaa agggcaaggt tccaaggcta 780
174 cagaatcaag catctccaac caatgtatgg cactgattat gaaatctgtg ctgtcagcag 840
175 accaactttt tgctccggga gtgaagatga tgaggacgaa cggtttcaat gcgtcgtaca 900
176 caacactggc agaaggggca aacattccga gcaagtacct aagacacatg aggaactgcg 960
177 gaggagtagc tctggacctg atgggaatga agaggatcaa aaactcacct gaaggagcca 1020
178 agtctaagat cttttccatc atccagaaga aagtaagagg aagatgtcgc acagaggagc 1080
179 aacgcctcct gactagcgca ctgaaaatca gcgacggtga aaacaagttc cagagaatca 1140
180 tggacactct atgtacaagc ttcttgattg accctccaag aactaccaa tgcttcattc 1200
181 cacctatttc cagtctcatg atgtacatcc aagaaggcaa ctctgtactg gcaatggatt 1260
182 tcatgaaacg cggagaggag gcctgcaaga tctgcagaga agccaaactg aaagtggggg 1320
183 taaacagtac gttcacaaatg tcagtagcta gaacatgcgt tgcagtgtca atgggttgcaa 1380
184 cagctttttg ttctgcagat atcatcgaga atgcagtgcc tggttccgaa aggtacagat 1440
185 ccaacatcaa ggctaacaca accaaaccaa aaaaggactc cacttacaca attcaaggac 1500
186 ttagattgtc taacgtgagg tatgaagcaa gacctgaaac atcacaaagc aacacagaca 1560
187 gaagttggca agtgaacgtg actgacagct tcggaggact tgctgtgttc aaccaagggg 1620
188 caattagaga aatgctagga gacggaacat cagagacaac tagtgtgaac gtcagagccc 1680
189 tggatgaagag aattctgaaa tcagcttcag agaggagtgc aagagctgta aagacattta 1740
190 tggatgggaga acaagggaaa tcagctattg ttatctctgg tgtgggactg ttctctattg 1800
191 actttgaagg ggtagaggaa gcggaaagga taactgacat gacacctgaa attgagtttg 1860
192 acgaggacga cgagggaagag gaagacattg acatttagag tgacaattat gtaactttct 1920
193 aattacccta tattgtttga atatataatg aaactattgt gtgttaaagg ttgtgggttt 1980
194 gattattaaa tttaaattga aacggtattg acgatatt 2018

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196 &lt;210&gt; SEQ ID NO: 4

197 &lt;211&gt; LENGTH: 616

198 &lt;212&gt; TYPE: PRT

199 &lt;213&gt; ORGANISM: Infectious Salmon Anaemia Virus

201 &lt;400&gt; SEQUENCE: 4

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202 Met Ala Asp Lys Gly Met Thr Tyr Ser Phe Asp Val Arg Asp Asn Thr
203 1 5 10 15
204 Leu Val Val Arg Arg Ser Thr Ala Thr Lys Ser Gly Ile Lys Ile Ser
205 20 25 30
206 Tyr Arg Glu Asp Arg Gly Thr Ser Leu Leu Gln Lys Ala Phe Ala Gly
207 35 40 45
208 Thr Glu Asp Glu Phe Trp Val Glu Leu Asp Gln Asp Val Tyr Val Asp
209 50 55 60
210 Lys Lys Ile Arg Lys Phe Leu Glu Glu Glu Lys Met Lys Asp Met Ser
211 65 70 75 80
212 Thr Arg Val Ser Gly Ala Val Ala Ala Ala Ile Glu Arg Ser Val Glu
213 85 90 95
214 Phe Asp Asn Phe Ser Lys Glu Ala Ala Ala Asn Ile Glu Met Ala Gly

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215          100          105          110
216 Val Asp Asp Glu Glu Ala Gly Gly Ser Gly Leu Val Asp Asn Arg Arg
217          115          120          125
218 Lys Asn Lys Gly Val Ser Asn Met Ala Tyr Asn Leu Ser Leu Phe Ile
219          130          135          140
220 Gly Met Val Phe Pro Ala Leu Thr Thr Phe Phe Ser Ala Ile Leu Ser
221 145          150          155          160
222 Glu Gly Glu Met Ser Ile Trp Gln Asn Gly Gln Ala Ile Ile Arg Ile
223          165          170          175
224 Leu Ala Leu Ala Asp Glu Asp Gly Lys Arg Gln Thr Arg Thr Gly Gly
225          180          185          190
226 Gln Arg Val Asp Met Ala Asp Val Thr Lys Leu Asn Val Val Thr Ala
227          195          200          205
228 Asn Gly Lys Val Lys Gln Val Glu Val Asn Leu Asn Asp Leu Lys Ala
229          210          215          220
230 Ala Phe Arg Gln Ser Arg Pro Lys Arg Ser Asp Tyr Arg Lys Gly Gln
231 225          230          235          240
232 Gly Ser Lys Ala Thr Glu Ser Ser Ile Ser Asn Gln Cys Met Ala Leu
233          245          250          255
234 Ile Met Lys Ser Val Leu Ser Ala Asp Gln Leu Phe Ala Pro Gly Val
235          260          265          270
236 Lys Met Met Arg Thr Asn Gly Phe Asn Ala Ser Tyr Thr Thr Leu Ala
237          275          280          285
238 Glu Gly Ala Asn Ile Pro Ser Lys Tyr Leu Arg His Met Arg Asn Cys
239          290          295          300
240 Gly Gly Val Ala Leu Asp Leu Met Gly Met Lys Arg Ile Lys Asn Ser
241 305          310          315          320
242 Pro Glu Gly Ala Lys Ser Lys Ile Phe Ser Ile Ile Gln Lys Lys Val
243          325          330          335
244 Arg Gly Arg Cys Arg Thr Glu Glu Gln Arg Leu Leu Thr Ser Ala Leu
245          340          345          350
246 Lys Ile Ser Asp Gly Glu Asn Lys Phe Gln Arg Ile Met Asp Thr Leu
247          355          360          365
248 Cys Thr Ser Phe Leu Ile Asp Pro Pro Arg Thr Thr Lys Cys Phe Ile
249          370          375          380
250 Pro Pro Ile Ser Ser Leu Met Met Tyr Ile Gln Glu Gly Asn Ser Val
251 385          390          395          400
252 Leu Ala Met Asp Phe Met Lys Asn Gly Glu Asp Ala Cys Lys Ile Cys
253          405          410          415
254 Arg Glu Ala Lys Leu Lys Val Gly Val Asn Ser Thr Phe Thr Met Ser
255          420          425          430
256 Val Ala Arg Thr Cys Val Ala Val Ser Met Val Ala Thr Ala Phe Cys
257          435          440          445
258 Ser Ala Asp Ile Ile Glu Asn Ala Val Pro Gly Ser Glu Arg Tyr Arg
259          450          455          460
260 Ser Asn Ile Lys Ala Asn Thr Thr Lys Pro Lys Lys Asp Ser Thr Tyr
261 465          470          475          480
262 Thr Ile Gln Gly Leu Arg Leu Ser Asn Val Arg Tyr Glu Ala Arg Pro
263          485          490          495

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VERIFICATION SUMMARY

DATE: 04/21/2006

PATENT APPLICATION: US/10/734,782A

TIME: 12:53:11

Input Set : A:\SEQLIST.TXT

Output Set: N:\CRF4\04212006\J734782A.raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date